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OM protein - protein search, using sw model

                        GenCore version 5.1.4_p5_4578
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Run on:                 March 14, 2003, 09:23:29 ; Search time 20.8151 seconds
                        (without alignments)
                        3900.178 Million cell updates/sec

Title:                  US-09-836-077-4
Perfect score:          2120
Sequence:               1 MTPPPGRAAPSAPRARVLS.........TFQVADSHPEVAQRVEPMGP 394

Scoring table:          BLOSUM62
                        Gapop 10.0 , Gapext 0.5

Searched:               671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:              671580

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length:  0
Maximum DB seq length:  2000000000
                 Listing first 45 summaries

Database :              SPTREMBL_21:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*
                15: sp_rvirus:*
                16: sp_bacteriap:*
                17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	907.5	42.8	653	12	Q64906	Q64906 alcelaphine
2	504	23.8	612	12	Q93F6	Q93F6 fowlpox vir
3	397	18.7	893	4	Q9C0B8	Q9C0B8 homo sapien
4	368.5	17.4	748	4	Q8TB71	Q8TB71 homo sapien
5	359.5	17.0	409	12	Q8QMR4	Q8QMR4 cowpox viru
6	354	16.7	635	4	Q96GX0	Q96GX0 homo sapien
7	352.5	16.6	754	4	Q8TDV7	Q8TDV7 homo sapien
8	346	16.3	963	4	Q9C0C4	Q9C0C4 homo sapien
9	345.5	16.3	416	12	Q98VP6	Q98VP6 vaccinia vi
10	342.5	16.2	775	11	Q90X23	Q90X23 mus musculu
11	326.5	15.4	457	4	Q9HBR1	Q9HBR1 homo sapien
12	320	15.1	756	13	Q8QGU9	Q8QGU9 gallus gall
13	316.5	14.9	782	4	Q9NS98	Q9NS98 homo sapien
14	308	14.5	1030	4	Q9H2E6	Q9H2E6 homo sapien
15	308	14.5	1049	4	Q9P2H9	Q9P2H9 homo sapien
16	300	14.2	1005	11	Q9EQ71	Q9EQ71 mus musculu

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17   298.5   14.1    418    4   Q96JU9   Q96JU9 homo sapien
18   296     14.0    761    4   Q8WUA9   Q8WUA9 homo sapien
19   281.5   13.3   1202    4   Q9P283   Q9P283 homo sapien
20   279     13.2    284   11   O54948   O54948 mus musculu
21   265.5   12.5   1022    4   Q9P249   Q9P249 homo sapien
22   264     12.5    724    4   Q9V7Q7   Q9V7Q7 drosophila
23   263     12.4    296   11   Q9JI29   Q9JI29 rattus norv
24   256.5   12.1    687    4   Q9BXR8   Q9BXR8 homo sapien
25   253     11.9    770    5   O44253   O44253 drosophila
26   253     11.9    770    5   O44253   O44253 drosophila
27   252     11.9    616    4   Q9V7P8   Q9V7P8 drosophila
28   251.5   11.9    367    4   Q9HAH9   Q9HAH9 homo sapien
29   248.5   11.7    963   11   Q91Y36   Q91Y36 rattus norv
30   240     11.3    935    4   Q96JF8   Q96JF8 homo sapien
31   229.5   10.8    923   11   Q8R4U3   Q8R4U3 mus musculu
32   225     10.6    920   11   Q8R4U4   Q8R4U4 rattus norv
33  218.5    10.3    228   12   Q9JF56   Q9JF56 vaccinia vi
34   212     10.0   1083    5   Q9VTT0   Q9VTT0 drosophila
35   207      9.8   1081    5   Q9U631   Q9U631 drosophila
36   186      8.8    676    5   Q9TYS4   Q9TYS4 caenorhabdi
37   169      8.0    658    5   Q95XP4   Q95XP4 caenorhabdi
38   165      7.8    658    5   Q9NI38   Q9NI38 caenorhabdi
39   160      7.5    264    5   Q95Q16   Q95Q16 caenorhabdi
40   137     10.0    951    5   Q8TA58   Q8TA58 caenorhabdi
41   131      6.2    620    1   Q98329   Q98329 molluscum c
42  127.5     6.0   1944    5   Q9N375   Q9N375 caenorhabdi
43   121      5.7    816    5   Q9V4A7   Q9V4A7 drosophila
44   121      5.7   2051    5   Q96682   Q96682 drosophila
45  115.5     5.4   1963    4   O75051   O75051 homo sapien
```

ALIGNMENTS

RESULT 1
Q64906

ID   Q64906   PRELIMINARY;   PRT;   653 AA.
AC   Q64906;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Similar to GENBANK ACCESSION number L26081.
DE   Alcelaphine herpesvirus 1 (wildebeest herpesvirus).
OS   Alcelaphine herpesvirus 1 (wildebeest herpesvirus).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=35252;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C500;
RX   MEDLINE=97404659; PubMed=261371;
RA   Ensser A., Pflanz R., Fleckenstein B.;
RT   "Primary structure of the alcelaphine herpesvirus 1 genome.";
RL   J. Virol. 71:6517-6525(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C500;
RA   Ensser A., Pflanz R., Fleckenstein B.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C500;
RX   MEDLINE=9720157J; PubMed=9049359;
RA   Ensser A., Fleckenstein B.;
RT   "Alcelaphine herpesvirus type 1 has a semaphorin-like gene.";
RL   J. Gen. Virol. 76:1063-1067(1995).
DR   EMBL; U18243; AAC54475.1; -.
DR   EMBL; AF005370; AAC58054.1; -.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
SQ   SEQUENCE   653 AA;   73645 MW;   5C2816BD567E706E CRC64;

Query Match   42.8%;   Score 907.5; DB 12; Length 653;
Best Local Similarity   48.9%;   Pred. No. 8.1e-71;

Matches 182; Conservative 54; Mismatches 129; Indels 7; Gaps 5;

```
Qy   22  PARFG-LPLRLRLLLVFWVAAASAQGHSRSGPRISAVWK----GQDHVDFSQFPHTVLFH   77
              ||:||| ||:| : ||||| : :|:::|||          |||||||:|
Db   45  PAAMGTLCVSIRLLMIL-SAITPAAKSRFIDKPRLIVNLTDGFGQ-HRFFGPQPHTVLFH  102

Qy   78  EPGSFSVWVGRGKGVHFNFPEGGKNASVRTVNIGSTKGSCQDKQDCGNYITLLERRGNGL  137
              |:|| ::|||||::|||||||||||||||||||||||||||| |||||||||| :||
Db  103  SLNSSDYVGVGNNTILFDFAHSSNASTALINITSTHNTHRLSSTCENFITLLHNQTDGL  162

Qy  138  LVCGTNARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGK  197
              | |||:||: ||||||::| :| |||:||||||||||||||||||||||| |||
Db  163  LACGTNSQKPSCW-LINNLITQFLGPKLGLAPFSPSSGGNLVLFDQNDTYSTINLYKSLSG  221

Qy  198  IPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNV  257
              ||||||||||||||| ::|||:|||||||||| :||||||||||||:|:|||||||
Db  222  SHKFRRIAGQVELYTSDTTAMHRPQFVQQATAVHKNESYDDKIYFFQENSHSDFKQFPHTV  281

Qy  258  SRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNRNRNRLQDVFLLPDPSGQWRDT  317
              || :|| :|||||||||| :| |:||| :||:| :|| |||:||||:| ||
Db  282  PRVGQVCSSDQGGESSLLSVYKWTTFLKARLACVDYDTGRIVNELQDIFIWQAPENSWEET  341

Qy  318  RVYGVFSNPWNYSAVCYSLGDIDRVFRTSSLKGYHMGLSNPRPGMCLPKKQPIPTETFQ   377
              |:||| |:|:| : |||:||||:|||||||:||| :: ||| ||| : |:|||||||
Db  342  LIYGLFLSPWNFSAVCVFTVKDIDHVFKTSKLKNYHHKLPTRPGQCMKNHQHVPITFQ   401

Qy  378  VADSHPEVAQRV  389
              ||||:|||:||
Db  402  VADRYPEVADPV  413
```

RESULT 2
```
ID   Q9J5F6      PRELIMINARY;     PRT;   612 AA.
AC   Q9J5F6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ORF FPV047 semaphorin vaccinia A39R homolog.
GN   FPV047.
OS   Fowlpox virus (FPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Avipoxvirus.
OX   NCBI_TaxID=10261;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20193820; PubMed=10729156;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT   "The genome of fowlpox virus.";
RL   J. Virol. 74:3815-3831(2000).
SQ   SEQUENCE   612 AA;  69514 MW;  175D0D18EC274E23 CRC64;
```

Matches 114; Conservative 57; Mismatches 107; Indels 30; Gaps 9;

Query Match 23.8%; Score 504; DB 12; Length 612;
Best Local Similarity 37.0%; Pred. No. 1.6e-35;

```
Qy   86  VGGRGKVYHFNFPEGGKNASV--RTVNIGSTKGSCQDKQDCGNYITLLERRGNGLLVCGTN  143
              :|| |: |||||||||||||  |:|||:||:||| ||||||:|||||:||||| |||||
Db   59  IGVNTNYVVVNTTDKSNITVDFSPDNVSTQSGA--------NYIFIGGYDDKILVCGTN  110

Qy  144  ARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRR  203
              |:|:|:| :| : | | | |:|| |  |: : |||||||||:|||:|||:| : | |
Db  270  DPAISRSQSLRPTKESSLNWLQDPAFVASAYIPESLGSSLQGDDDKIYFFSETGQEFEF  329
```

RESULT 3
```
ID   Q9C0B8      PRELIMINARY;     PRT;   893 AA.
AC   Q9C0B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   KIAA1745 protein (Fragment).
GN   KIAA1745.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082932; PubMed=11214970;
RA   Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XIX.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:347-355(2000).
SQ   SEQUENCE   893 AA;  98361 MW;  D6C6C48DEE524F14 CRC64;
```

Query Match 18.7%; Score 397; DB 4; Length 893;
Best Local Similarity 30.1%; Pred. No. 6.6e-26;
Matches 129; Conservative 54; Mismatches 167; Indels 78; Gaps 16;

```
Qy    3  PPPPGRAAPSAPRARVL----------------------SLPARFGLPLRLRLLLVF-   41
              |||||  : : |                        ||||:||||||||||||||
Db    3  PPEPEPRDTVAPALRMLRTAMGLRSWLAAPWGALPPPRPLLLLLLLLLLQPPPPTWALS  101

Qy   42  ASAQGHSRSGPRISAVWKGQDHVDFSQPEP----------HTVLFHEPGSFSVWVGRGKVYHFN  96
              | : :||| |:|||||| |||||||||          |:| |||||::|||||||||||||
Db  102  ----------PRIS-LPLGSEERPFLREAEHISNYTALLSRDGRTLVGAREALFALS  150

Qy   97  -----FPEGKNASVRTVNIGSTKGSCQDK-----QDCGNYI-TLLERRGNGLLVCGTNAR  145
              |||||||||||||:||||||||||     |||||||  ||||||||||||||||||||
Db  151  SNLSFLPGGEYQELLWGADAEHKQQCCSFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAF  210

Qy  146  KPSCW--NLVNDSVV-----MSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGK  197
              |||||  ||||||||     ||||||||||||||||||||||||||||:|||:|||:|
Db  211  SPMCTYINMENFTLARDEKGNVLLEDGKGRCPFDPNFKSTALVVDGELY-TGTVSSFQGN  269

Qy  198  IPRFRRIRGESELYTSDTV--MQNPQFIKATIVHQD----QAYDDKIYYFFREDNPDKNP  251
              |||||||||||||||||||  |||||||||||||||    ||||||||||||||||:||
Db  270  DPAISRSQSLRPTKESSLNWLQDPAFVASAYIPESLGSSLQGDDDKIYFFSETGQEFEF  329
```

Right column continuation:

Matches 182; Conservative 54; Mismatches 129; Indels 7; Gaps 5;

```
Db  111  SSSPTPCW-YINGTIKEPTPYGRGLSPESYDMTGLVLIDGKEIYSTIKK-YSHLSTGFSR  167

Qy  204  IRGESELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQL  263
              |||||||||||||||||||||||||||||||||||||||||||||||:||||  : :|
Db  168  IVGKRPVLYTSSSTMKNPKEVHLVSLQETNSINDTIYIFFQEE-----GMAKVSRV  217

Qy  264  CRGDQGGESSLSVSKWNTFLKAMLVCSDAATNRNRNRLQDVFLLPDPSGQWRDTRVYGVF  323
              ||||||||||||||||||||||:||||||||||||||||||||||| :|||||||||
Db  218  CKHDGGSGCGSLSGSKWSTFLKSIMICED--LNVRFNYLKDVVVIKGKSP--NFIIYGLF  273

Qy  324  SNPWNYSAVCYSLGDIDRVFRTSSLKGYHMG--LSNPRPGMCLPKKQPIPTETFQVADSH  382
              |||||||||||||||||:||||:||||| |   ||  || |||| |:|||||| :|
Db  274  FNEWNYSAVCMFKFDKIQNNFNTSPLKGYSGGKVLSVRPGTCL--NTSTPRDTFEVIDLY  331

Qy  383  PEVAQRVE  390
              |::| ||
Db  332  PETLYGVK  339
```

```
Qy     252 EAPLNVSRVAQOLCRGDQGGESSLSVSKWNTFLKAMLVGSDAATNRNFNRLQDVFLLPPDS 311
               |:||:||:|:||:||    ||  ||||||||| |||| | ||| | ||  ||||||| ||
Db     330 FENTIVSRIARICKGDEGGGERVLQ-QRWTSFLKAQLLCSRPDDGFPENVLQDVFTLSPSP 388

Qy     312 GQWRDTRVYGVFSNPWNY------SAVCVYSLGDIDRVF------------RTSSLKGYHMGLS 357
               |||| | |||||||           :  |||||| |||               |||||||||:|:
Db     389 QDWRDTLPFYGVFTSQWHRGTTEGSAVCVFTMKQVRVFSGLIYKEVNRETQQWTVTHPVP 448

Qy     358 NPRPGMCL 365
               |||||||:
Db     449 TRPRPGACI 456
```

RESULT 4

Q8TB71

```
ID      Q8TB71;    PRELIMINARY;     PRT;     748 AA.
AC      Q8TB71;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Hypothetical 83.0 kDa protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=MUSCLE;
RA      Strausberg R.;
RL      Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC024220; AAH24220.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE   748 AA;   83034 MW;  587C53CB65AB4656 CRC64;
```

```
Query Match              17.48%;    Score 368.5;  DB 4;   Length 748;
Best Local Similarity    29.0%;      Pred. No. 1.6e-23;
Matches    127; Conservative    49; Mismatches  167;  Indels    95;  Gaps    18;
```

```
Qy       7 GRAAPSAPRARVLSLPARFGLPLRLRLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDF 66
              || | | | ::||   |  ||  ||| |  | | |||
Db      22 GSAAPSPPRLRL--------------------------------SFQEELQA-WHQLQTFSL 49

Qy      67 SQPEPHIVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNI----------G 111
             |  |  || | |  |     || ||| |||||||||||||| |               |
Db      50 ERTCCYQALLVDEERGRLFVGAEHNVASLNL---DNISKRAKKLAWPAPVEWREECNWAG 106

Qy     112 STKGSCQDKQDCGNYITLLER-RGNGLLVCGTNARKPSC-----WNLVNDSVVM----SL 161
              ||| || |  ||| |     :|| |:| |                :|   |   : |
Db     107 KDIGT---ECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRI 161

Qy     162 GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPFRFIRGESELYT-SDTVMQ 218
              |:|  | ||| |   ||   || :  : :|    | |:|:|      |  :| ||
Db     162 EDGKGKSPYDPRIRAASVLVGEELYSGVAADLMGRDFYIFRSLGQRPSLRTEPHDSRWLN 221

Qy     219 NPQFIKA-TIVHQDQAYDDKIYFFREDNPDKNPE-APLNVSRVAQOLCRGDQGGESSLSV 276
              ||| :|   |  ||||| ||||||   |||||:  |||||||||:|||||||||||||
Db     222 EPKFVKVFWIPESENPDDDKIYFFRETAVEAAPALGRLSVSRVGQOICRNDVGGQRSL-V 280

Qy     277 SKWNTFLKAMLVCS--DAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNP--WNYSAV 332
              ||||||||||||   |||||||||||||||| |||| ||||||  | || ||    ||
Db     281 NKWTTFLKARLVCSVPGVEGDTFPDQLQDVFLL--SSRDHRTPLLYAVFSTSSIFQGSAV 338

Qy     333 CVYSLGDIDRVF------------RTSSLKGYHMGLSNPRPGMCLPKK----QPIPIET 375
              ||||||| |||               ||||||||  | |||||  ||          || ||
Db     339 CVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFSSSTKDFPDDV 397

Qy     376 FQVADSHPEVAQRVEPMG 393
              | |||| |||  |  | |
Db     398 IQFARNHPLMYNSVLPTG 415
```

RESULT 5

Q8QMR4

```
ID      Q8QMR4;    PRELIMINARY;     PRT;     409 AA.
AC      Q8QMR4;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      V169.
OS      Cowpox virus (CPV).
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Orthopoxvirus.
OX      NCBI_TaxID=10243;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RX      MEDLINE=83117629; PubMed=6961398;
RA      Pickup D.J.; Bastia D., Stone H.O., Joklik W.K.;
RT      "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT      repeated and unique sequence elements.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RX      MEDLINE=90177240; PubMed=2309453;
RA      Parsons B.L., Pickup D.J.;
RT      "Transcription of orthopoxvirus telomeres at late times during
RT      infection.";
RL      Virology 175:69-80(1990).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RX      MEDLINE=91196263; PubMed=2014645;
RA      Hu F.Q., Pickup D.J.;
RT      "Transcription of the terminal loop region of vaccinia virus DNA is
RT      initiated from the telomere sequences directing DNA resolution.";
RL      Virology 181:716-720(1991).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RX      MEDLINE=94378510; PubMed=8091665;
RA      Hu F.Q., Smith C.A., Pickup D.J.;
RT      "Cowpox virus contains two copies of an early gene encoding a soluble
RT      secreted form of the type II TNF receptor.";
RL      Virology 204:343-356(1994).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RA      Pickup D.J.;
RL      Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
RN      [6]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRIGHTON RED;
RA      Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
RL      Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF482758; AAM13617.1; -.
SQ      SEQUENCE   409 AA;   46488 MW;  E14438F5EC68F6F8 CRC64;
```

```
Query Match              17.0%;    Score 359.5;  DB 12;   Length 409;
Best Local Similarity    30.4%;      Pred. No. 4.2e-23;
Matches    95; Conservative    53; Mismatches  129;  Indels    35;  Gaps    11;
```

```
Qy      84 VWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSCQDKQDCGNYITLLERRGNGLLVCGTN 143
             :|  ||||||||||||||||||||| |:|:|| || || || || ||||:|| ||||||
Db      36 LYTGVNGAVTFSNNELNKTGLTNNNYITTSIKVEDKD------------TLVCGTN 80

Qy     144 ARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPFRFR 203
             ||| |  |||| |  : | |: | || |||||||||||||:|||||||||: |  |:|:|
Db      81 NGNPKCWKIDGSEDPKHRG--RGYAPYQKSKVTIISYNGC-VLSDINISKEG--IKRWRR 135

Qy     204 IRGES--ELYTSDTVMQNPQFIKATIVHQDQAYDDKIYFFREDNPDKNPEAPLNVSRVA 261
             | || |:| |||| |  || | |:| | ||:|||||||||||||| ||| | | |||| | |
Db     136 FDGPCGYDLYTADNVIPK-DGVRGAFVDKDGTY-DRVYILFTDTIGSKR---IVKIPYIA 190

Qy     262 QLCRGDQGGESSLSVSKWNTFLKAMLVCS-DAATNRNFNRLQDVFLLPDPSGQWRDTRVY 320
             ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db     320
```

```
Db    191  QMCLNDEGGPSSLSSHRWSTFLKVELECDIDGRSYRQI--IHSKTIKTD-----NDTILY 243
           |:|  ||||       | ::| |||:  ||   |  : : :     ||   ||
Qy    321  GVFSNPWNYSAVCVYSLGDIDRVFRTSSLKGYHMGLSNPRPGMCLPKKQPIPTETFQVAD 380

Db    244  VFFDSPYSKSALCAYSMNSIKQSFTTSKLEGYTKQLPSPAPGICLPAGKVVPHTTFEVIE 303
           |:|||| :::::|
Qy    381  SHPEVAQRVEPM 392

Db    304  KYNVLDDIIKPL 315
```

RESULT 6
Q96GX0

ID   Q96GX0   PRELIMINARY;   PRT;   635 AA.
AC   Q96GX0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Unknown (protein for MGC:18122).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009113; AAH09113.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF01403; Sema; 1.
SQ   SEQUENCE   635 AA;   70694 MW;   D994099B476B9210 CRC64;

Query Match   16.7%; Score 354; DB 4; Length 635;
Best Local Similarity   34.1%; Pred. No. 2.4e-22;
Matches 104; Conservative 39; Mismatches 122; Indels 40; Gaps 13;

Qy   125 NYITLLER-RGNGLLVCGTNARKPSC----WNLVNDSVVM----SLGEMKGYAPFSPDE 174
           |::| ||| |||||||||| |::: |:||||||:| | |: | |
Db   2 NFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRIEDGKGKSPYDPRH 61

Qy   175 NSLVLFEGDEVYYSTIRKQEYNGKIPREFRIRGESELYT---SDTVMQNPQFIKA-TIVHQ 230
           :|| |||:||||| :|| | ||||:| |||: | ||| | |:| ||| ||||
Db   62 RAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLNEPKFEVKVFWIPES 121

Qy   231 DQAYDDKIYFFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVC 289
           | | ||||||||||||||||| ||||||||||||||:|:|:||||||| ||||| |:|
Db   122 ENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-VNKWTTFLKARLVC 180

Qy   290 S--DAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNP--WNYSAVCVYSLGDIDRVF- 344
           : ::|||||||| :::| ||||||| |||||:|||| |||||||||||||||||||
Db   181 SVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYAVFSTSSIFQGSAVCVYSMNDVRRAFL 238

Qy   345 ------RTSSLKGYHMGLSNPRGMCLPKK--------QPIPTETFQVADSHPEVAQR 388
                 |||||||||||||||||| |||| ||||||||||||||||||||
Db   239 GPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFPSSTKDFPDDVIQFARNHPLMYNS 297

Qy   389 VEPMG 393
           | ||
Db   298 VLPTG 302
```

RESULT 7
Q8TDV7

ID    Q8TDV7          PRELIMINARY;     PRT;     754 AA.
AC    Q8TDV7;
DT    01-JUN-2002 (TrEMBLrel. 21, Created)
DT    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    Semaphorin 3B.

GN    SEMA 3B.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Koyama N.;
RT    "semaphorin 3B (SEMA3B) cDNA.";
RL    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AB083186; BAB88870.1; -.
SQ    SEQUENCE   754 AA;   83691 MW;   E61FD08C04E9A68E CRC64;

Query Match             16.6%;  Score 352.5;  DB 4;  Length 754;
Best Local Similarity   28.4%;  Pred. No. 4.1e-22;
Matches  126;  Conservative  50;  Mismatches  167;  Indels  101;  Gaps  19;

```
Qy      7  GRAAPSAPRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDF 66
           | |||   |       | ::  ||| :  :||  | :|:|  :|: :      : |:|
Db     22  GSAAPSPPRLRL--------------------------------SFQELQA-WHGLQTFSL 49,

Qy     67  SQPEPHTVLFEHEPGGSFSVWWGGRGKVYHFNFPPEGKNASVRTVNI--------G 111
           :||| |||||  |  |  | | | :: |  |:||| |::   |  |           |
Db     50  ERTCCYQALLVDEERGRLFVGAENHVASLNL--DNISKRAKKLLAWPAPVEWREECNWAG 106

Qy    112  STKGSCCQDKQDCGNYITLLER-RGNGLLVCGTNARKPSC----WNLVNDSVVM---SL 161
           ||:|:|  | ||||||||||||| |||||||||||||||       |:||||||:|    |
Db    107  KDIGT-----ECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRI 161

Qy    162  GEMKGYAPFSPDENSLVLFEGDEVYYSTIRKQEYNGKIPREFRIRGESELYT---SDTVMQ 218
           |:|||:|||||| ||:|| |||:||||||| || |||:| |||:|||||||    || |:|
Db    162  EDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLN 221

Qy    219  NPQFIKA-TIVHQDQAYDDKIYFFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSV 276
           ::|:| |  |||| |  | ||||||||||||||||| ||||||||||||||:|:|:||||||
Db    222  EPKFEVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-V 280

Qy    277  SKWNTFLKAMLVCS--DAATNRNFNRL------QDVFLLPDPSGQWRDTRVYGVFSNP--- 326
           |||||||||| |:|  ::|||||||||        :|||| :::|  ||||||:|||
Db    281  NKWTTFLKARLVCSVPGVEGDTHFDQLRFPFAEDVFLL--SSRDHRTPLLYAVFSTSSSI 338

Qy    327  WNYSAVCVYSLGDIDRVF----------------------RTSSLKGYHMGLSNPRGMCLPKK------Q 369
           |||||||||||||||||                       |||||||||||||||||| ||||      |
Db    339  FQGSAVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFPSSTK 397

Qy    370  PIPTETFQVADSHPEVAQRVEPMG 393
           ||||||||||||||||||||||||
Db    398  DFPDDVIQFARNHPLMYNSVLPTG 421
```

RESULT 8
Q9CQC4

ID   Q9CQC4   PRELIMINARY;   PRT;   963 AA.
AC   Q9CQC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   KIAA1739 protein (Fragment).
GN   KIAA1739.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082932; PubMed=11214970;
RA   Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XIX.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:347-355(2000).
DR   EMBL; AB051526; BAB21830.1; -.
DR   InterPro; IPR003599; Ig.

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DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002165; Plexin_repeat.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01437; PSI; 1.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00423; PSI; 1.
FT   NON_TER   1
SQ   SEQUENCE   963 AA;  106735 MW;  3FA37DBBA3483ECE CRC64;

Query Match        16.3%;  Score 346;  DB 4;  Length 963;
Best Local Similarity   25.7%;  Pred. No. 2.2e-21;
Matches  127;  Conservative  55;  Mismatches 177;  Indels 136;  Gaps 19;

Qy   11 PSAP---RARVLSLPARFGLPLRLRL------------------------------ 33
Db   64 PEVPLTLRARAISLMASSGRKLWLRYPSFLPAAWICLLPGWERLGRPRWGCQCQORLFQKC 123

Qy   34 ----------LLVFWVA----------AASAQGHSRSGPRISAVWKG---------- 63
Db  124 PLLPIRGFGWHLLVAWGAGSRGARLRAVEPQGSCPSAAMLTPAELATVVRRFSQTGIQDF 183

Qy   64 VDFSQPEPHTVLFHEPGSEPSVVWGGRGKGKVYHENPP------------------- 109
Db  184 LTLTLTEPFGLLY--------VGAREALFAFSMEALELQGAISWEAPVEKKTECIQ--- 231

Qy  110 IGSTKGSCQDKQDCGNYITLLE-RRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEM---K 165
Db  232 ----KGK-NNQTCFNFRFLQPYNASHLYVCGTYAFQPKCTYVNMLTFTLEHGEFEDGK 286

Qy  166 GYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV---MQNPQF 222
Db  287 GKCPYDPAKGHAGLLVDGELYSA-TLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNEPHF 345

Qy  223 IKATIVHQD----QAYDDKIYYFFREDNDPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSK 278
Db  346 VGSAVPESVGSFTGDDDKVYFPREERAVESDCYAEQVVARVARVCKGDMGGARTLQ-RK 404

Qy  279 WNTFLKAMLVCSDAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWN---YSAVCVY 335
Db  405 WTTFIKARLACSAPNWQLYFNQLQAMHTLQDTS--WHNTFFGVFQAQWGDMVLSAICEY 462

Qy  336 SLGDIDRVPRTSSLKGYHM--------GLSNPRPGMCL----------PKKQPIPTETF 376
Db  463 OLEEIQRVFE-GPYKEYHEEAQKWDRYTDPVPSPRPGSCINNWHRRHGYTSSLELPDNIL 521

Qy  377 QVADSHPEVAQRVEP 391
Db  522 NFVKHPLMEEQVGP 536


RESULT 9
ID   Q98VP6                PRELIMINARY;    PRT;    416 AA.
AC   Q98VP6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Semaphorin.
GN   A39R.
OS   Vaccinia virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10245;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BUFFALOPOX;
RA   Gardner J.D., Tscharke D.C., Reading P.C., Smith G.L.;
RT   "Evidence of a Pro-Inflammatory Role for Vaccinia Virus Semaphorin
RT   A39R.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ309297; CAC37361.1; -.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
SQ   SEQUENCE   416 AA;  47125 MW;  AFE77F24678F94B5 CRC64;

Query Match        16.3%;  Score 345.5;  DB 12;  Length 416;
Best Local Similarity   31.1%;  Pred. No. 7.2e-22;
Matches   98;  Conservative   52;  Mismatches 126;  Indels 39;  Gaps 14;

Qy   84 VWVGGRGKVYHFNFPEGKNASVRTVNIGSTKGSCSQDKQDCGNYITL---LERRGNGLLVC 140
Db   36 LYTGVNGAVTFS----NNKLNKT---GLTN------------NNYITTSIKVEDADKDTLVC 79

Qy  141 GTNARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPR 200
Db   80 GTNNGNPKCWRIDGSDDDPKHRG--RGYAPYQONSKYTIISHNGC-VLSDINISKEG--IKR 134

Qy  201 FRRIRGES--ELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNDPDKNPEAPLNVS 258
Db  135 WRRFDGPCGYDLFTADNVIPK-DGLRGAFVDKDGTY-DKVYILFTDTIGSKR---IVKIP 189

Qy  259 RVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS-DAATNRNFNRLQDVFLLPDPSGQWRDT 317
Db  190 YIAQMCLNDEGGPSSLSSHRMSTFLKVELECDIDGRSYRQI--IHSRTIKYD----NDT 242

Qy  318 RVYGVFSNPWNYSAVCVYSLGDIDRVFRTSSLKGYHMGLSNPRPGMCLPKKQPIPTETFQ 377
Db  243 ILYFFDSPYSKSALCTYSMNTIKQSFSTSKLEGYTKQLPSPAPGICLPAGKVVPHTTFE 302

Qy  378 VADSHPEVAQRVEPM 392
Db  303 VIEKYNVLIDDIIKPL 317


RESULT 10
ID   Q90X23                PRELIMINARY;    PRT;    775 AA.
AC   Q90X23;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Semaphorin M-Semak.
GN   SEMA3E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57/BLACK 6;
RA   Miyazaki N., Furuyama T., Inagaki S.;
RT   "A novel semaphorin, M-Semak which inhibits neural outgrowth from
RT   sensory neurons.";
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF034744; AAD01996.1; -.
DR   MGD; MGI:1340034; Sema3e.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00423; PSI; 1.
SQ   SEQUENCE   775 AA;  89543 MW;  221E2766F40409BD4 CRC64;

Query Match        16.2%;  Score 342.5;  DB 11;  Length 775;
Best Local Similarity   28.3%;  Pred. No. 3.2e-21;
Matches  126;  Conservative  65;  Mismatches 160;  Indels 95;  Gaps 23;

Qy   13 APRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWKGQODHVD----FSQ 68
Db    2 APAGHILTL-----LLWGHLLELWTPGHSA---NPSYPRLRLSHKELLELNRISIFQS 51
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Qy    69  P-----EHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNIGST------KG   115
              |||:|                                            ||
Db    52  PLGFLDLHTMLLDEYQE-RLFVGGRDLVYSLNL-ERVSDGYREIYWPSTAVKVEECIMKG  109

Qy   116  SCQDKQDCGNYITLLER-RGNGLLVCGTNARKPSCWNLVNDSVVMSLGEM-------     164
          :::|:  |:||   | |:|  ||  | |     |       | |   |
Db   110  -KDANECANYIRVLHYNRTHLLTCATGAFDPHC-----AFIRVGHHSEEPLFHLES     160

Qy   165  ------KGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFR----RIRGESELYT    212
                :|   | |:| | :|| | | :     |      |      |:||:|
Db   161  HRSERGRGRCPFDPNSSFVSTLVGNELFAGLYSDYGRDSAIFRSMGKLGHIRTE---HD   217

Qy   213  SDTVMQNPQFIKATIVHQDQAYD-D-KIYYFEREDNPDKNPEAPLNVSRVAQLCRGDGQGGE 271
          ::    :  |:  ::|  :  |  | |:|:|:   :::|  :    : | |  | |:  ||
Db   218  DERLLKEPKFVGSYMIPDNEDRDDNKMYFFFTEKALEAENNAHTIYTRVGRLCVNDMGGQ   277

Qy   272  SSLSVSKWNTFLKAMLVCSDAATN----RNFNRLQDYVFLLP--DPSGQWRDTRVYGVF--- 323
          ::| ::|| |||| :|||   |       |:|||||:|||||   | | |||:|||| |
Db   278  RLL-VNKWSTFLKARLVCSVPGMNGIDTYFDELEDVFLLPTRDP---KNPVIFGLFNTT    332

Qy   324  SNPWNYSAVCVYSLGDIDRVFR-----TSSLKG--YHMGLSN------PRPGMCLPK----- 367
          ||   : ||||| :  | | |        |  |          | |     ||||
Db   333  SNIFRGHAVCVYHMSSIREAFNGPYAHKEGPEYHWSLYEGKVPYPRPGSCASKVNGGKYG   392

Qy   368  -KQPIPTETFQVADSHPEVAQRVEPM                                    392
           |  |  :   |     :|:|
Db   393  TTKDYPDDAIRFARMHPLMYQPIKPV                                    418


RESULT 11
Q9HBR1
ID   Q9HBR1              PRELIMINARY;       PRT;    457 AA.
AC   Q9HBR1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 50.4 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA   Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA   Yu J., Han L.H.;
RL   "Novel Human cDNA clones with function of inhibiting cancer cell
RL   growth.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF217991; AAG17234.1; -.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 457 AA; 50413 MW; 7EBCACE81295C388 CRC64;

Query Match       15.4%;   Score 326.5;  DB 4;  Length 457;
Best Local Similarity   28.2%;   Pred. No. 3.8e-20;
Matches 119;  Conservative  47;  Mismatches 165;  Indels  91;  Gaps  18;

Qy     7  GRAAPSAPRARVLSLPARFGLPLRLLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDF    66
          | |||   ||:| ||                              :|
Db    22  GSAAPSPPRLRL----------------------------------SFQELQA-WHGLQTFSL  49

Qy    67  SQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNI----------------G 111
          :   |  :| | | | |  | |     |: :          |
Db    50  ERTCCVQALLVDEERGRLFVGAENHVASLNL---DNISKRAKKLAMPAPVEWREECNWAG   106

Qy   112  STKGSCSQDKQDCGNYITLLER-RGNGLLVCGTNARKPSC----WNLVNDSVVM------SL 161
              |   :      ||::  | | |  ||| ||| |  :|        |:|
Db   107  KDIGT----ECMNFVKLLHAYNRTHLLACGTGAFIPTCAFVEVGHRAEEPVLRLDPGRI   161

Qy   162  GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQ  218
```

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Db   162  EDGSKGKSPYDPRIHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLN 221

Qy   219  NPQFIKA-TIVHQDQAYDDKIYFFREDNPDKNPE-APLNVSRVAQLCRGDGQGGESSLSV    276
          :| |:|  ||:||: |::||||| ||:: |:::| |||:||| | |||:|:|||:|| ::|
Db   222  EPKFVKVFNIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQGRSL-V  280

Qy   277  SKWNTFLKAMLVCS--DAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNP--WNYSA    331
          :||:|||||:|||||    |||||||||||||||   |:|| | | : |:|     ::||
Db   281  NKWTTFLKARLVCSVPGVGEVGDTHFDQLQDVFLL--SSRDHRTPLLIYAVFSTSSIFQGSA 338

Qy   332  VCVYSLGDIDRVF------RTSSLKGYHMGLSNPRPGMCLPKK---QPIPTETFQVA     379
          ||||| : : ||       | ||: :     : : ||  |        |    | |
Db   339  VCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRQA-CAPARPLAPSVPPRTSQTM   397

Qy   380  DS     381
          :|
Db   398  SS     399


RESULT 12
Q8QGU9
ID   Q8QGU9              PRELIMINARY;       PRT;    756 AA.
AC   Q8QGU9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Semaphorin 3F.
GN   SEMA3F.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Watanabe Y., Nakamura H.;
RT   "Axon guidance of the trochlear nerve by Sema 3F along mid-hindbrain
RT   boundary.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB072930; BAB88691.1; -.
SQ   SEQUENCE 756 AA; 85196 MW; C36754C02541ED88 CRC64;

Query Match       15.1%;   Score 320;  DB 13;  Length 756;
Best Local Similarity   28.0%;   Pred. No. 2.9e-19;
Matches 119;  Conservative  64;  Mismatches 156;  Indels  86;  Gaps  24;

Qy    33  LLLVFWVAAASAQGHSRSG----PRISAVWK-----GQDHVDFS---QPEPHIVLFHEPG    80
          |  : |:||                ||:| |     |||| |    :||||:| | | |
Db    12  LITLGWRAA-----HGKDGVPPPPRVQLSFKELKATGTAHF-FNFLLNSSDYRLLKDED    65

Qy    81  SFSVWVGGRGKVYHFNFPEGKN-------ASVRTVN-IGSTKGSCQDKQDCGNYITLL     130
          | |  | |     |: :          :||||||| |||:||||  | ||||||:|:
Db    66  HDRMVGSKDYVLSLDLHDINREPLIIHWPASGQRIEECILSGKNS----NGECGNFIRLI   122

Qy   131  ER-RGNGLLVCGTNARKPSC-----WNLVNDSVVM---SLGEMKGYAPFSPDENSLVLF    180
          :  |||  :|||| | :|     |:|: |          | | | ||:|||  |::
Db   123  QPWNRTHLYVCGTGAYNPICAFINRGRKAQDYIFYLEPDKLESGKGKCSYDPKVDTVSAL   182

Qy   181  EGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV---                      235
          | :|||  : : :  |      :|   |:|:
Db   183  INEELYAGV-YIDFMGTDAAIFRTMGKQTAMRTDQYNSRWLNDPAFVRAQLIPDSSERND  241

Qy   236  DKIYYFEREDNPDKNPEAPLN--VSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS--   290
          ||:|:|:||     |  ||| ||:|| | ||||:|| |||||:||||||||||:|||||
Db   242  DKLYFFFRE----KSADAPLSPGVYSRIGRICLNDDGGHCCL-VNKWSTFLKARLVCSVP  296

Qy   291  -DAATNRNFNRLQDVFLLPDPSGQWRDTR---VYGVFS---NPWNYSAVCVYSLGDIDRV   343
           |  |   | | |||||:    |:| |  :|   : |:|   |||:|||||||| || ||
Db   297  GPDGIETHFDELQDVFI----QQTQDTKNPVIYAVFSASGSVFKGSAVCVSMADIRMV    351

Qy   344  FRT--SSLKG------YHMGLSNPRPGMC------LPKKQPIPTETFQVADSHPEVA     386
          | |  ||: :       : : ||  |||       |::  |    | |
```

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Db    352 FNRPFAHKEGPNYQWMPYTGKMPYPRPGTCPGGTFTPSMKSTKDYPDEVINFMRSHPLMY 411

Qy    387 QRVEP 391
          | ||
Db    412 HAVYP 416
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RESULT 13
ID    Q9NS98
AC    Q9NS98; Q9H7O3;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    Semaphorin sem2 (FLJ00014 protein).
GN    SEM2 OR FLJ00014.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.,
RA    Saito T.;
RL    "Human semaphorin.";
RL    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN    [2]
RP    SEQUENCE OF 58-782 FROM N.A.
RC    TISSUE=SPLEEN;
RA    Ohara O., Nagase T., Kikuno R., Okumura K.;
RT    "The nucleotide sequence of a long cDNA clone isolated from human
RT    spleen.";
RL    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AB024296; BAA98132.1; -.
DR    EMBL; AK024425; BAB15715.1; -.
DR    Pfam; PF01403; Sema; 1.
DR    Pfam; PF00047; ig; 1.
DR    InterPro; IPR003599; Ig.
DR    InterPro; IPR003600; Ig_like.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003659; Plexin-like.
DR    InterPro; IPR001627; Sema.
DR    SMART; SM00409; IG; 1.
DR    SMART; SM00410; IG_like; 1.
DR    SMART; SM00423; PSI; 1.
SQ    SEQUENCE 782 AA; 85700 MW; 85CB424874DF6663 CRC64;
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Query Match             14.9%;   Score 316.5;  DB 4;  Length 782;
Best Local Similarity   27.2%;   Pred. No. 6.2e-19;
Matches 125;   Conservative 57;   Mismatches 144;   Indels 133;   Gaps 24;

Qy      4 PPPGRAAPSAPARARV------------------------------LSLPARRGLPLRLRLLLVFWVAAAS 43
          |:||     |||||         ||:| :|| |: : | ||
Db     24 PSPG---PSVPRLRLSYRDLLSANRSAIFLGPOGSLNLQAMYLDEYRDRLFLGGLDALYS 80

Qy     44 AQGHSRSGPRISAVWKGQDHVDFSQPEPHTVLF-HEPGSFSVWVGGRGKVYHFNFPEGKN 102
          |:|           ||| |:|||||||| |      |: ||||:|||||||:|||||||
Db     81 L---------------------PDPREVLWPPQPGQ-----------------RE 103

Qy    103 ASVRTVNIGSTKGSCQDKQDCGNYITLLE-RRGNGLLLVCGTNARKPSCWNLVNDSVVMSL 161
          || |||||||||||||||||||| ||| | |||| |||||||||||||||||||||||||
Db    104 ECVR------KGR-DPLTECANFVRVLQPHNRTHLLACGTGAFQPTC-----ALITV 148

Qy    162 GEM-------KGTAPFSPDENSLVLFEGDEVYSTIRKEYNGKIPRFRIRG 206
          |||        ||| ||||||||||||||||||||||||||||||||||
Db    149 GHRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGL-TADFLGREAMIFRSGG 207

Qy    207 ESELYTSD------TVMQNPQFIKATIVHDQAYD-DKIYYFFREDNPDKNPEAPLN---VSR 259
          |:|||||       |::| ||:|| :|||||:  |||||||||||||||||||||    |||
Db    208 PRPALRSDSDQSLLHDRFVMAARIPENSDQONDKVYFFFSETVP--SPDGGSNHVTVSR 265

Qy    260 VAQLCRGDQGGESSLSVSKWNTFLKAMLVCS----DAATNRNFNRLQDVFLLPDPSGQWRD 316
          | :||   |||||||||||||||||||||||      :|  | ||     |:|  :
Db    208 PRPALRSDSDQSLLHDRFVMAARIPENSDQONDKVYFFFSETVP--SPDGGSNHVTVSR 265
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Db    266 VGRVCVNDAGGQRVL-VNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAG--KS 322

Qy    317 TRVYGVFSN--PWNYSAVCVYSLGDIDRVPR---------TSSLKGYHMGLSNRPGMC 364
          || :||   :||| ||||||||||||||||             |  || |:||| ||
Db    323 LEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPOHQWGPYGGKVFFPRPGVC 382

Qy    365 LPKK----QP---------------IPTETFQVADSHPEVAQRVEP 391
          |  |    :|               :||||||||||:|||:|||||
Db    383 -PSKMTAQPGRPFPGGSTKDYPDEVLQFARAHPLMFWPVRP 420
```

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RESULT 14
ID    Q9H2E6
AC    Q9H2E6;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
DT    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE    Semaphorin SEMA6A1.
GN    Semaphorin SEMA6A1.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=20564339; PubMed=10993894;
RA    Klostermann A., Lutz B., Gertler F., Behl C.;
RT    "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-
RT    1/Sema6A-1) bind to the Enabled/vasodilator-stimulated Phosphoprotein-
RT    like Protein (EVL) via a novel carboxyl-terminal zyxin-like domain.";
RL    J. Biol. Chem. 275:39647-39653(2000).
DR    EMBL; AF279656; AAG29378.1; -.
DR    InterPro; IPR003659; Plexin-like.
DR    InterPro; IPR001627; Sema.
DR    Pfam; PF01403; Sema; 1.
DR    SMART; SM00423; PSI; 1.
SQ    SEQUENCE 1030 AA; 114368 MW; A57B79C10AEC4B34 CRC64;
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Query Match             14.5%;   Score 308;  DB 4;  Length 1030;
Best Local Similarity   26.0%;   Pred. No. 5.1e-18;
Matches 109;   Conservative 61;   Mismatches 165;   Indels 84;   Gaps 17;

Qy      6 LLLYFTLLHEPAGAGFPEDSSPISI-----SHGNTYKQYP-VFVGHKPGRNTTQRIRLDIQ 59
          |||| |     | ||   |  |    |           | | :| |  |  |  | |:| |
Db      6 LLLYFTLLHEPAGAGFPEDSSPISI-----SHGNTYKQYP-VFVGHKPGRNTTQRIRLDIQ 59

Qy     33 LLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDFSQPEPHTVLFHEPG--------- 80
          |||||| |      | |  |  || || |   |  ||   |  | |
Db     81 MIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSRQADVDTCRMKGKHKDECHN 119

Qy     81 ------SFSVWVGGRGKVYHFNFPEGKNASV---------RTVNIGSTKGSCQDKQDCGN 125
                | ||||:|||||||:|||||||  |            || ||||||||||||||||
Db     60 MIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSRQADVDTCRMKGKHKDECHN 119

Qy    126 YI-TLLERGNGLLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYA--PFSPDENSLVLFEG 182
          || |||| | |||||||||||||||||||||||||||||| |     |:||||||| |
Db    120 FIKVLLKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD 179

Qy    183 DEVYS-------TIRKQEYN--GKIPRFRRIRGESELYISDTVMQNPQFIKATIVHDQDA 233
          ||| |        ||: |:   |||| ||  | ||| |||||:|||||:||| |:|||||
Db    180 GKLYSATVVDFLAIDAVIYRSLGESPTLRTVKHDSKW-----LKEPYEVQAV-----D 227

Qy    234 YDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGGESSLSVSKWNTFLKAMLVCS-DA 292
          | |||||||||||||||||||||:||||||||||||| |||||||||||||||||||| ||
Db    228 YGDVIYYFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG 287

Qy    293 ATNRNRNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY---SAVCVYSLGDIDRVPRTSSL 349
          || | | ||||||||||||||||| |||||||||||     |||| |||||||||| ||:
Db    288 DSHYFNILQAVTDVIRING--RDV-VLATFSTPYNSIPGSAVCAYDMDIASVP-TGRF 343

Qy    350 KGYHM--------GLSNPRGMC------LPRKQPIPTETFQVADSHPEVAQRV 389
          |||           ||||||:       |||: |:||||||||||:||::|||
Db    344 KEQKSPDSTWTPVPDERVPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAV 402
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RESULT 15
Q9P2H9
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ID   Q9P2H9
AC   Q9P2H9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   KIAA1368 protein (Fragment).
GN   KIAA1368.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes.XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
DR   EMBL; AB037789; BAA92606.1; -.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00423; PSI; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   1049 AA;  116511 MW;  7781D20ACC7A8AEA CRC64;
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Query Match            14.5%;    Score 308;  DB 4;  Length 1049;
Best Local Similarity  26.0%;    Pred. No. 5, 2e-18;
Matches  109; Conservative  61; Mismatches 165;  Indels  84;  Gaps  17;

Qy     33 LLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDFSQPEPHTVLFHEPG------------ 80
             ||||||||||||||||||||||||||||
Db      8 LLLYFTLLHFPAGAGFPEDSEPISI------SHGNYTKQYP-VFVGHKPGRNTTQRHRLDIQ 61

Qy     81 -----SFSVWVGGRGKVYHFNFPEGKNASV------------------RTVNIGSTKGSCODKQODCGN 125
               ::::: |||  | ||                  ::.:||   |  :.||  |
Db     62 MIMIMNGTLYIAARDHIYTVDIDISHTEEIYCSKKLTWKSRQADVDTCRMKGKHKDECHN 121

Qy    126 YI-TLLERGNGLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYA--PFSPDENSLVLFEG 182
            || |||||| |||| ||||||  || || ||: ||            :: ||
Db    122 FIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD 181

Qy    183 DEVYS-------TIRKQEYN--GKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQA 233
            ::|             ::|   : ||: ::|| : :: :: ||             ::
Db    182 GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKW-----LKEPYEVQAV-----D 229

Qy    234 YDDKIYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS-DA 292
            |||:|| ||:|| ||   ||||: ::||.|   :||    :: :: | |||||||||||| ::
Db    230 YGDVIYFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSELKARLNCSVPG 289

Qy    293 ATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY---SAVCVYSLGIDRVFRTSSL 349
            |: :|| |||| ||| |||  || ||| |||| ::: :  | ||: ||||| ||||||| |
Db    290 DSHFYFNILQAVTDVIRING--RDV-VLATFSTPYNSIPGSAVCAYDMLDIASVF-TGRF 345

Qy    350 KGYHM------------GLSNPRPGMC-------LPKKQPIPTEFQVADSHPEVAQRV 389
             ::           :   |||| :                :|| |:|||:||| :::
Db    346 KEQKSPDSTWTPVPDERVKPRPGCCAGSSSLERYATSNEEFPDDTLNFIKTHPLMDEAV 404
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Job time : 26.8151 secs
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